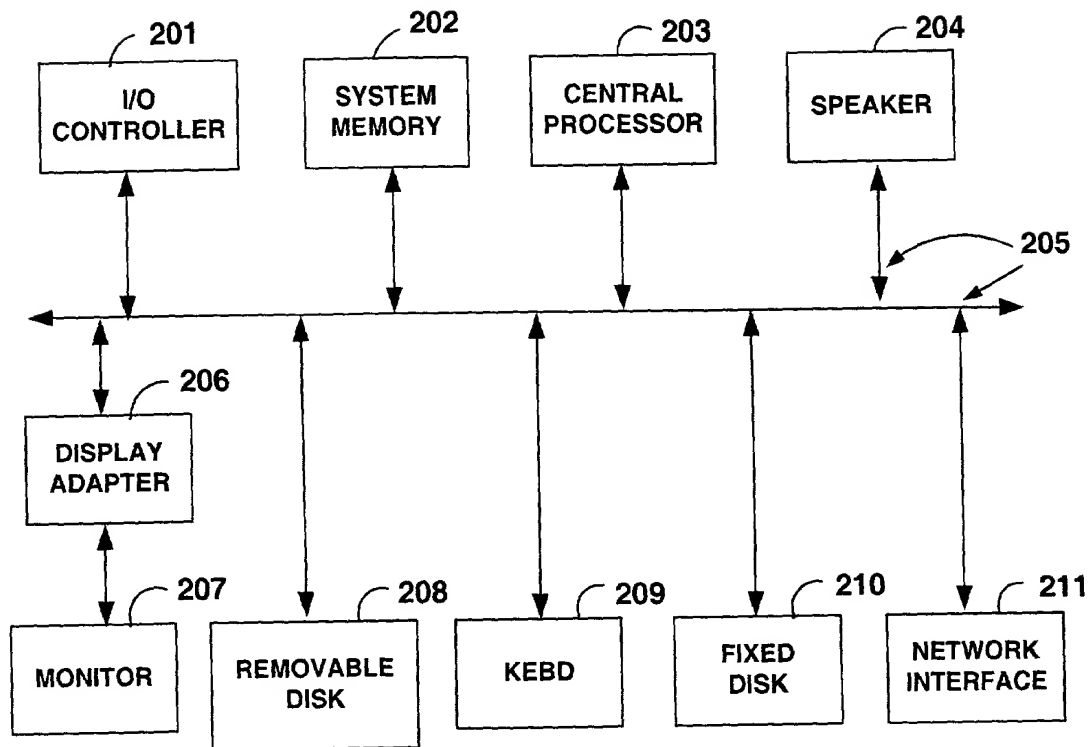


**Figure 1**

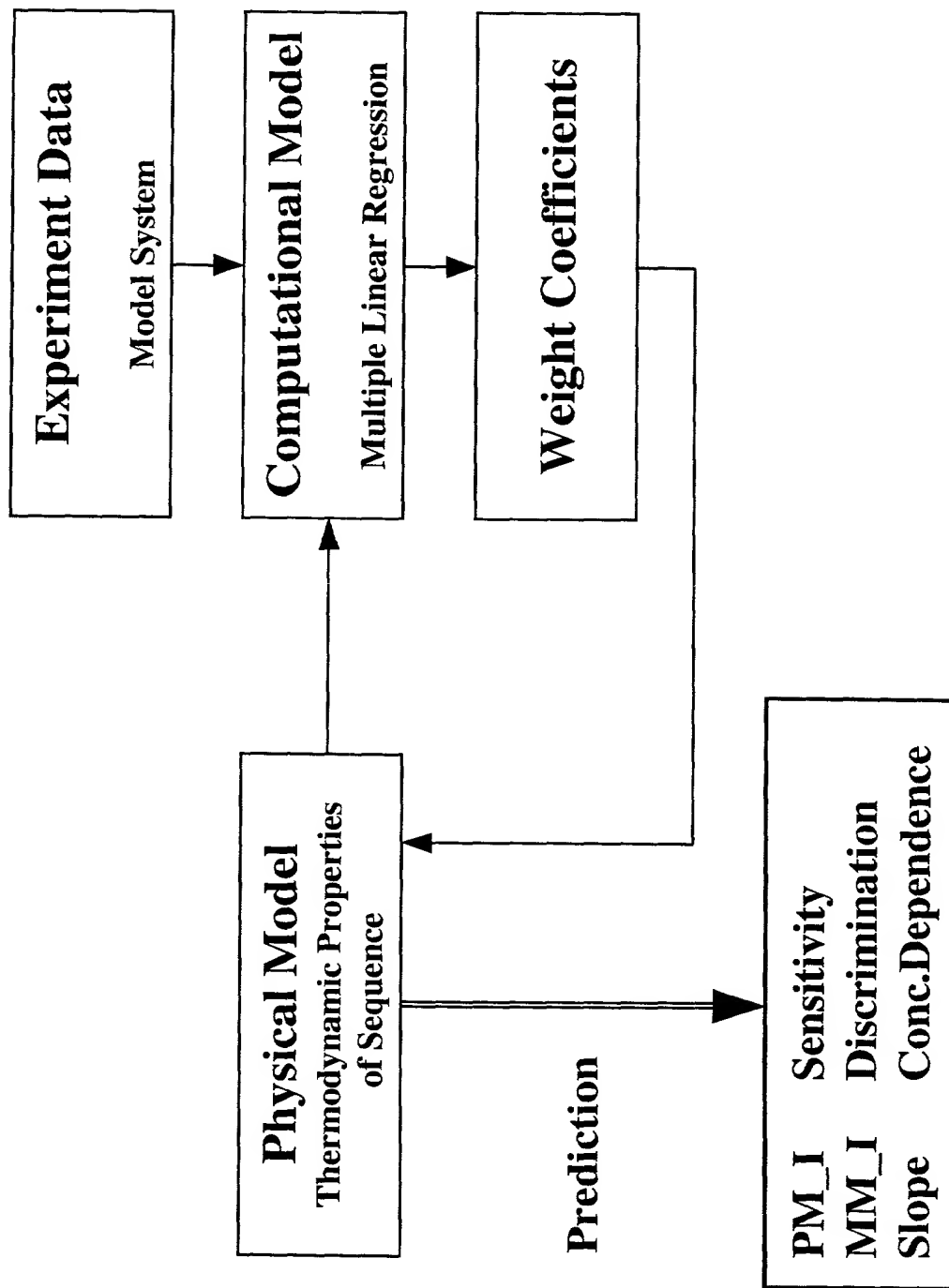


**Figure 2**

0012227" 535514260

# Predicting Probe Quality

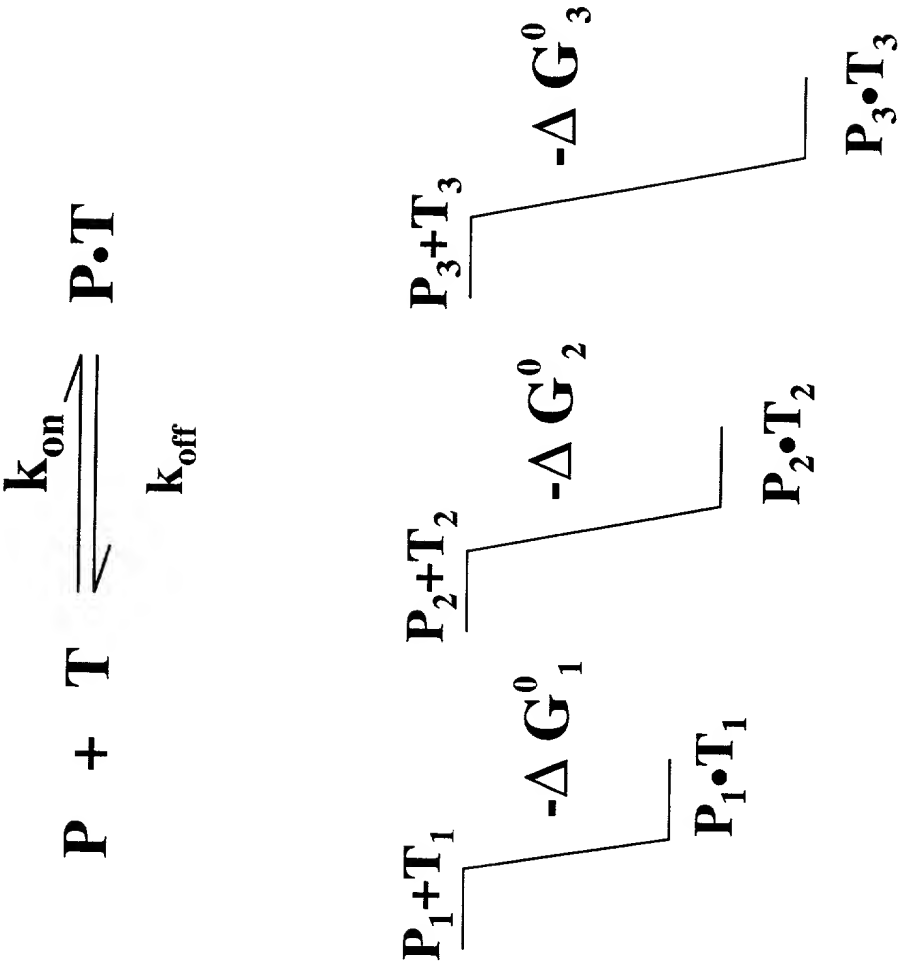
Figure 3



037227" 59534460

# Basic Physical Model

Figure 4



DOCKET # 3373.1

# Define Each Nucleotide at Each position

Figure 5

Example : GTCA

\*Using A as ref. 3 base/position

<u>i</u>	<u>Position</u>	<u>Base</u>	<u>S<sub>i</sub></u>
1	1	C	0
2	1	G	1
3	1	T	0
(1 <sup>st</sup> position is G)			
4	2	C	0
5	2	G	0
6	2	T	1
(2 <sup>nd</sup> position is T)			
7	3	C	1
8	3	G	0
9	3	T	0
(3 <sup>rd</sup> position is C)			
10	4	C	0
11	4	G	0
12	4	T	0
(4 <sup>th</sup> position is A as reference)			

# Relative $\Delta G$ vs. Base Position

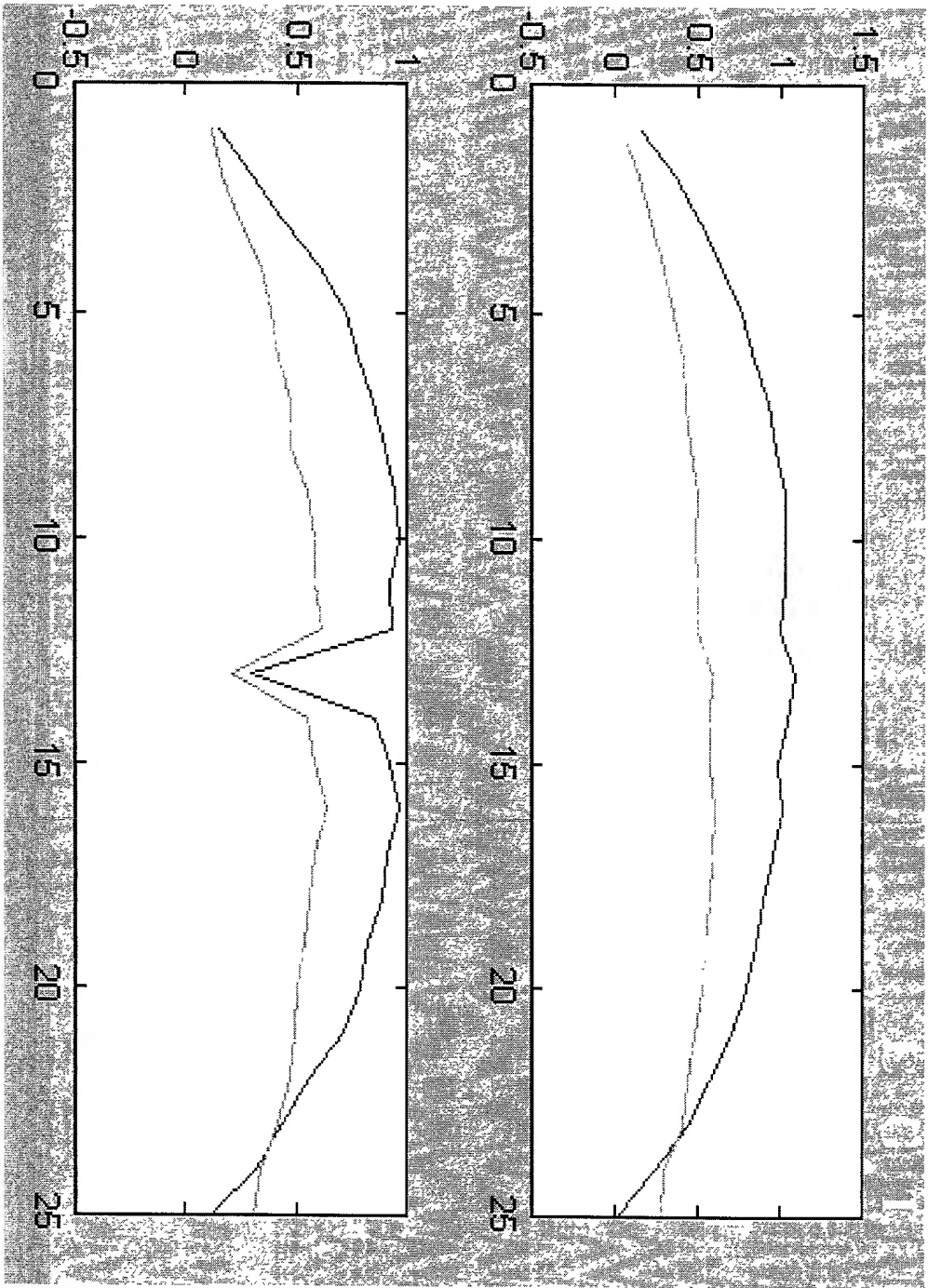


Figure 6A

PM

Figure 6B

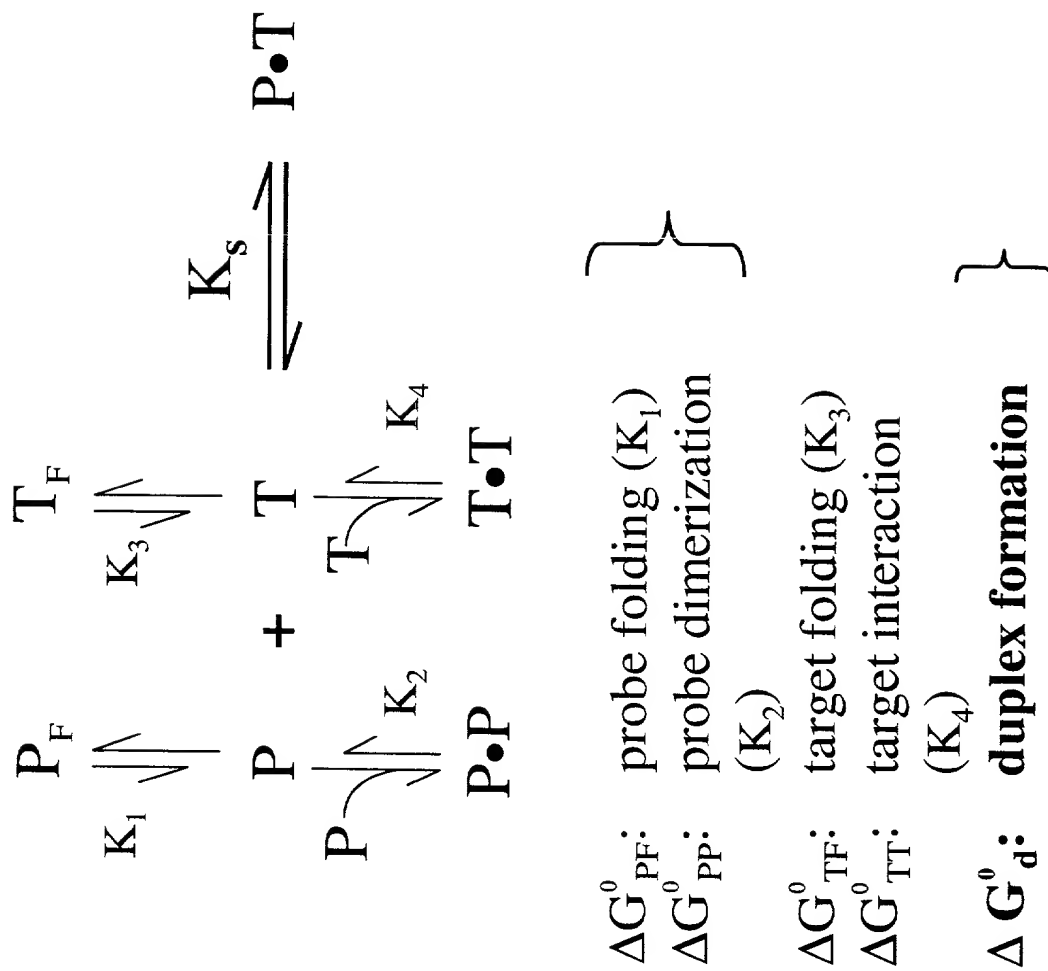
MM

Base Position in Probe Sequence

0 5 10 15 20 25

## Figure 7

# Overall Reaction



# Concentration Dependence: Slope

Figure 8

$$\ln I = S \cdot \ln C + \ln K_{app}$$

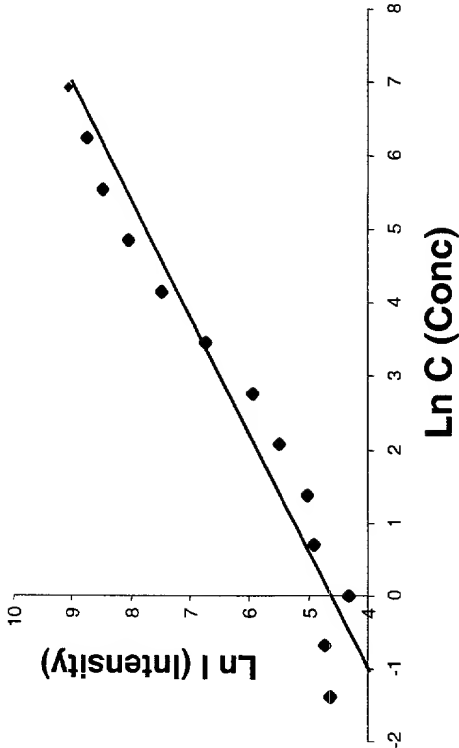
$$I = K_{app} \cdot C^S$$

**I:** Intensity

**K<sub>app</sub>:** Apparent Affinity Constant

**C:** Concentration

**S:** Empirical Value (0 < S <1)





# Relationship between Kapp vs. S

- Prediction of Probe Saturation

Figure 9A

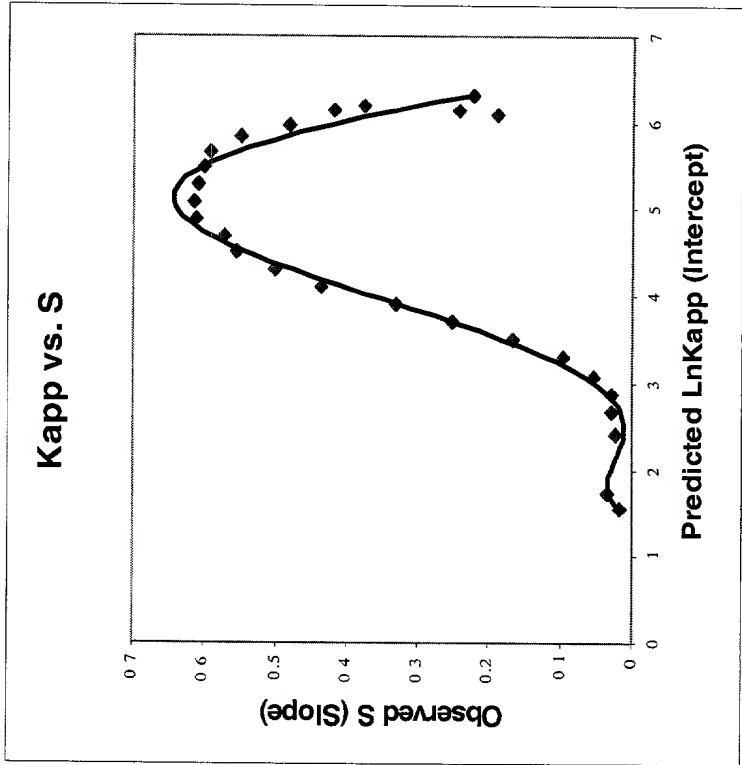
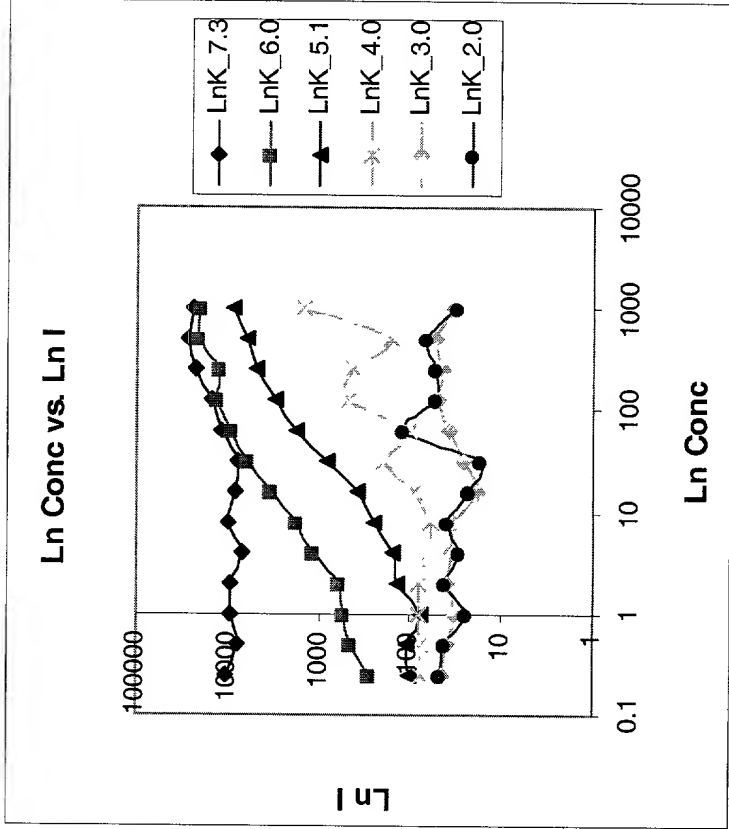


Figure 9B



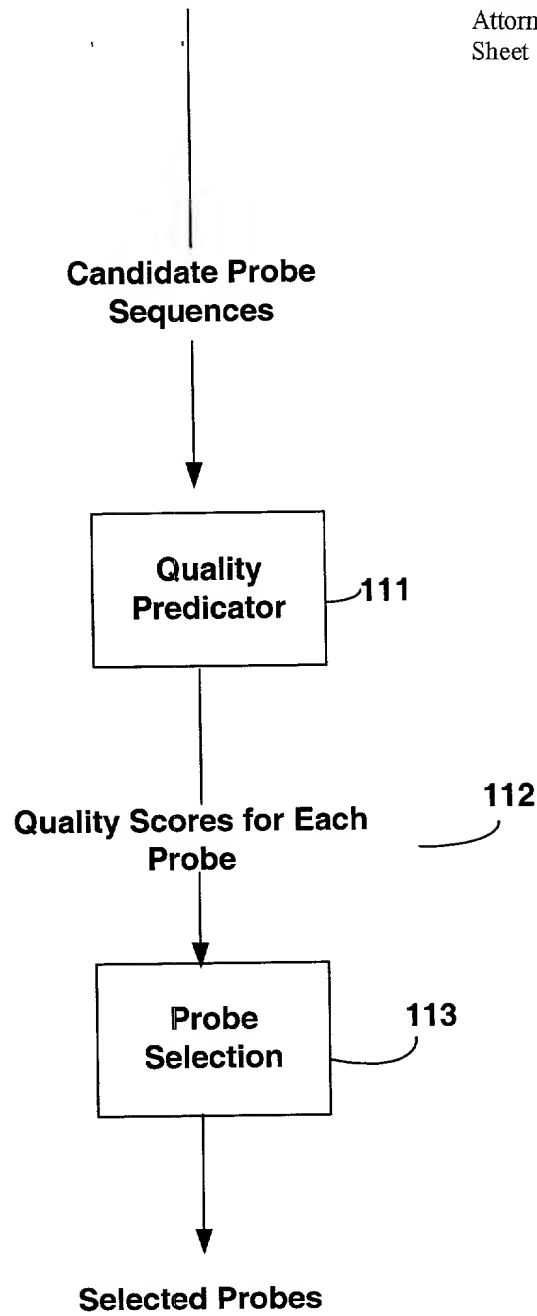


Figure 10

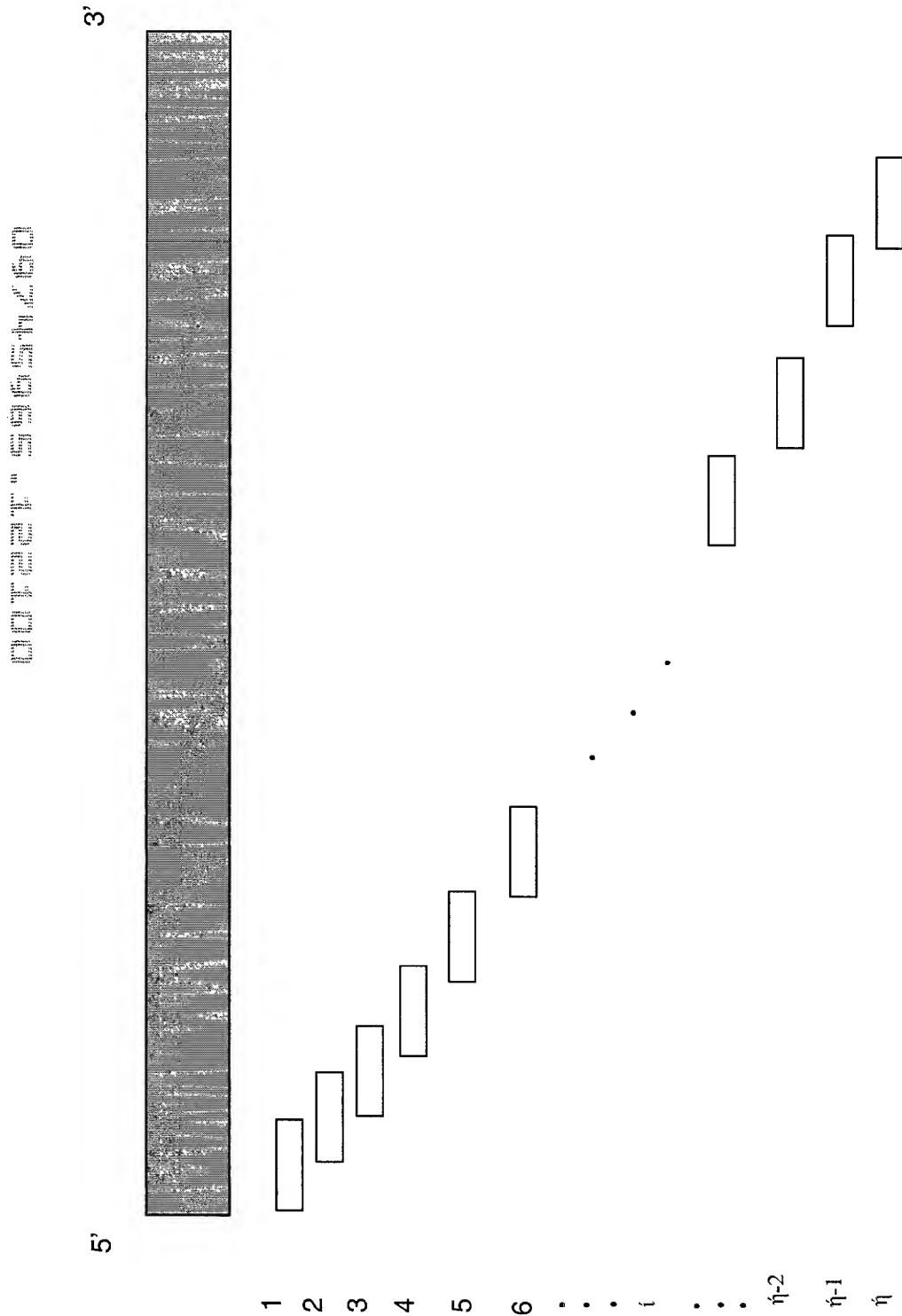


FIGURE 11

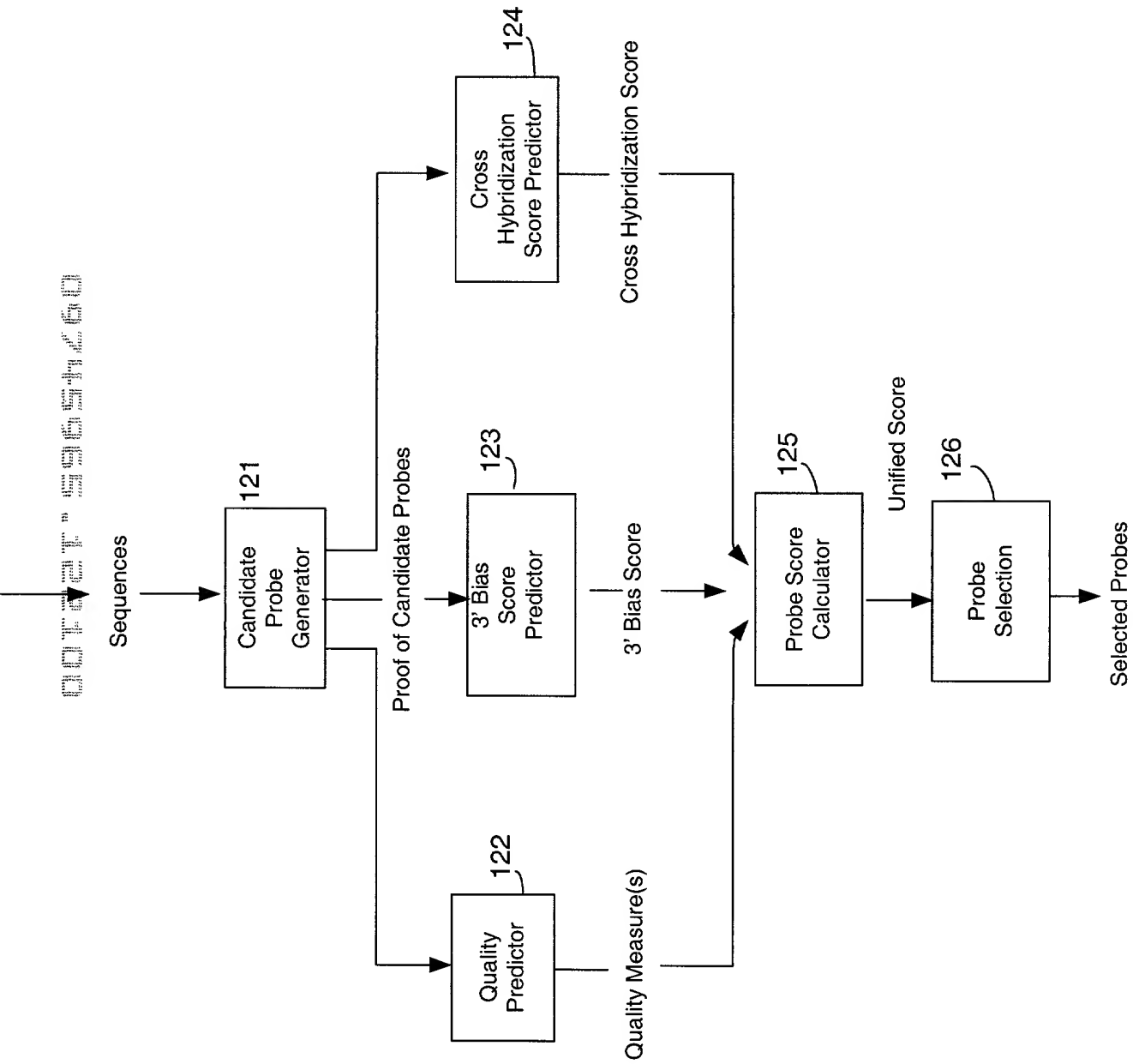
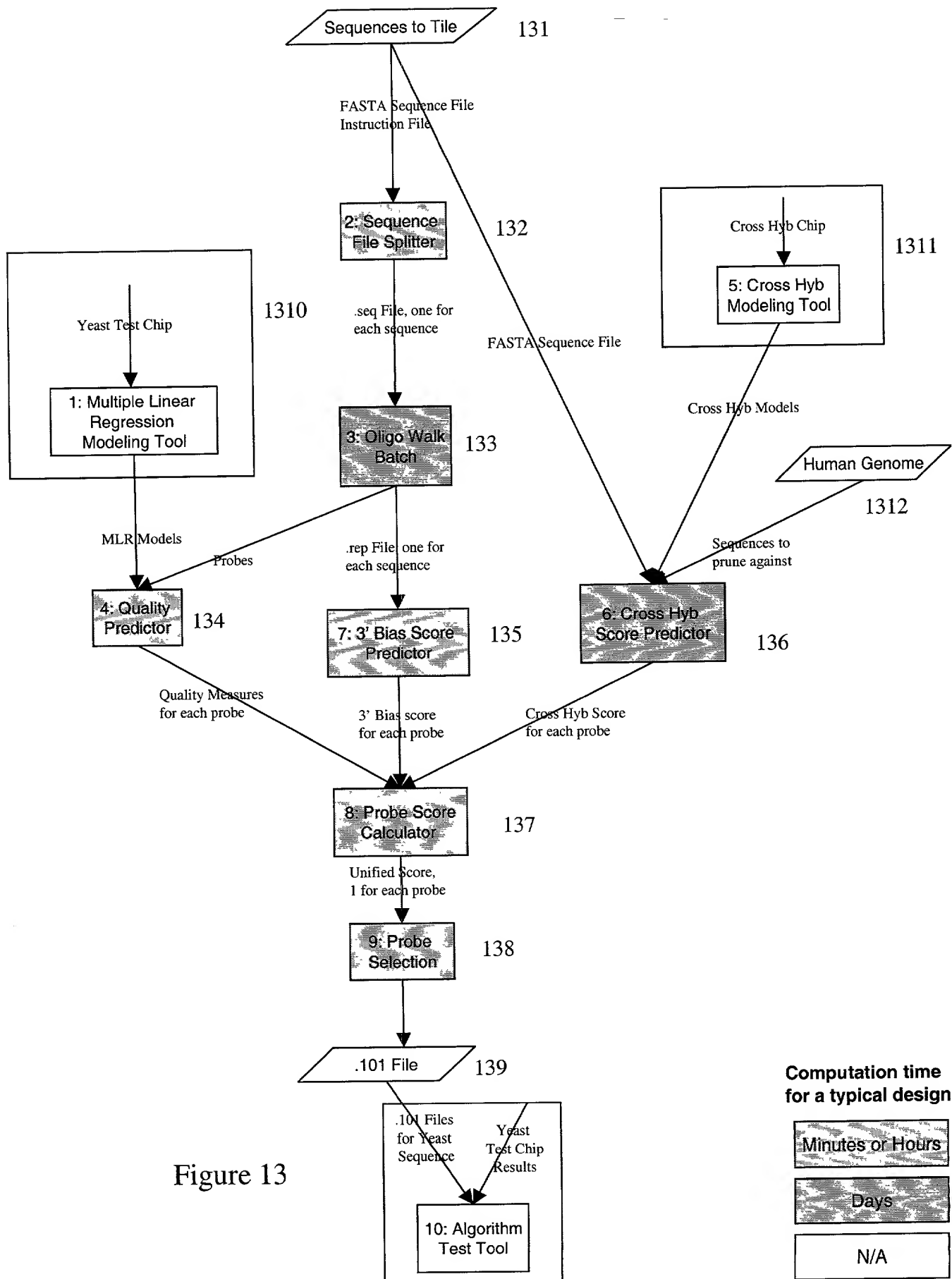


Figure 12

004595-100



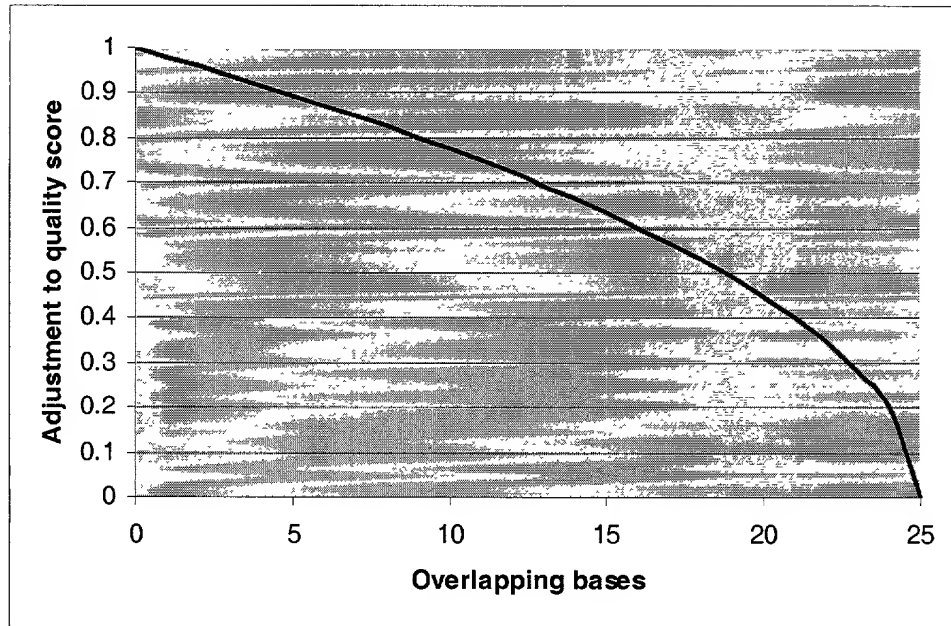


Figure 14

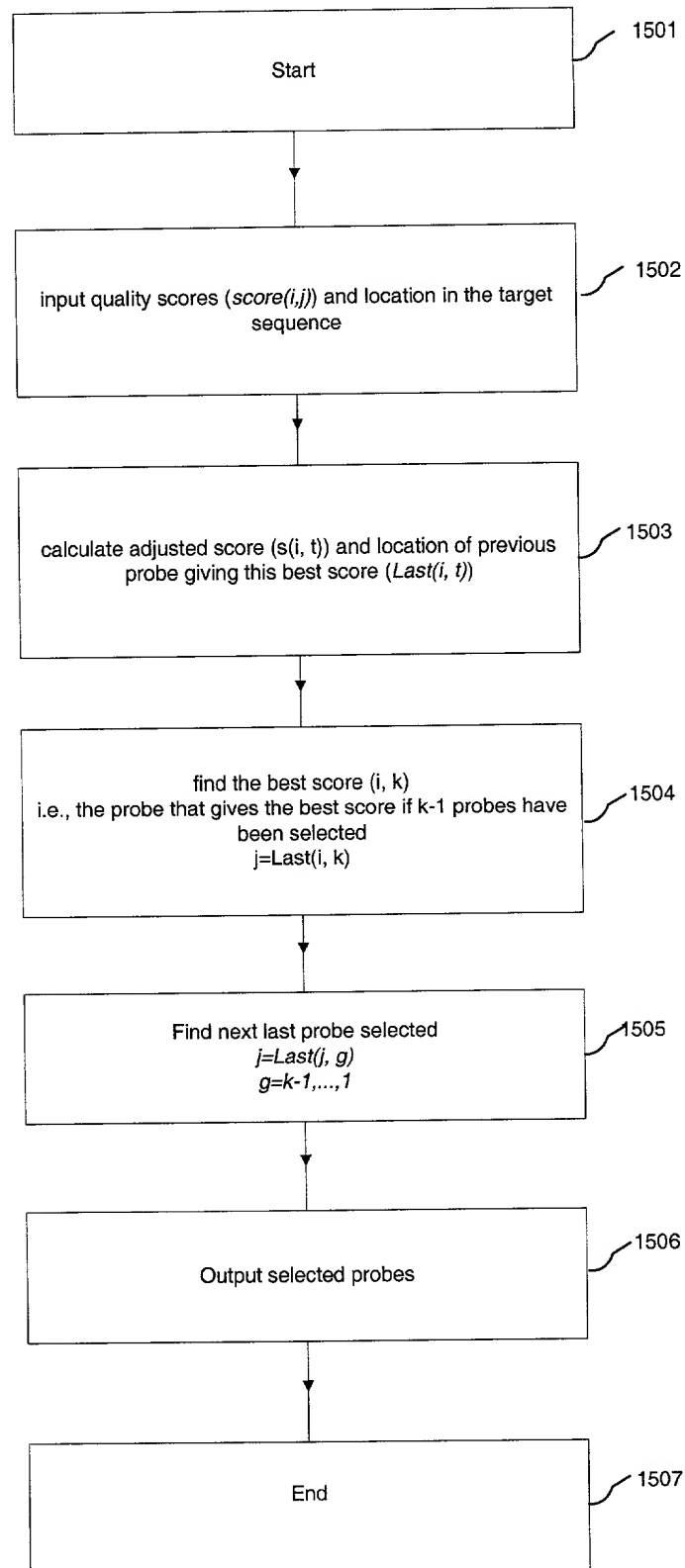


Figure 15

OUTLET" SEVENTH

# Latin Square MLR

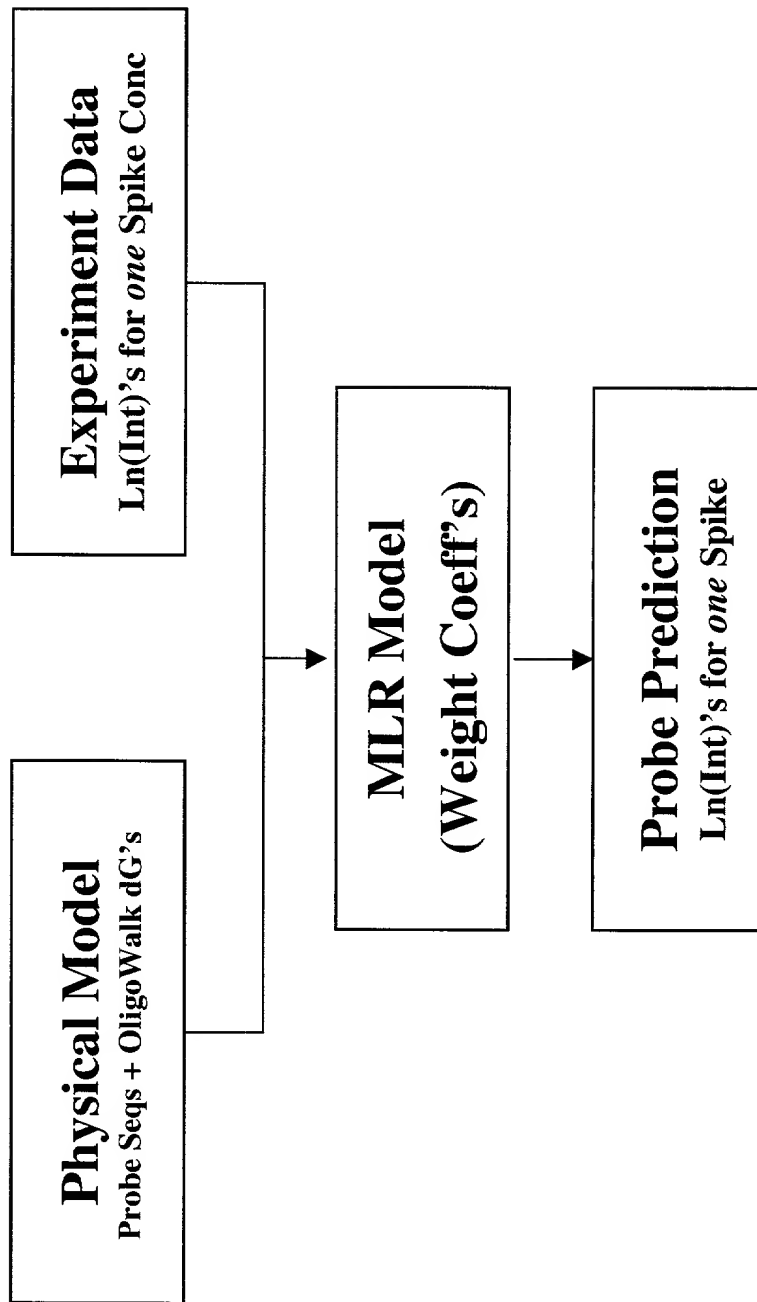


Figure 16



# 112 Yeast Clones Randomly Divided into 14 Groups

## Groups

1	2	3	4	5	6	7	8	9	10	11	12	13	14
YNL259C	YNL037C	YAL038W	YHR044C	YMR127C	YLR377C	YOL064C	YPL209C	YIR034C	YJR148W	YEL046C	YGR185C	YBR166C	YOL165C
YEL003W	YDR113C	YLR083C	YJL117W	YNL290W	YOL086C	YJR094C	YFL029C	YMR276W	YML060W	YGR072W	YGL181W	YJL155C	YNL227C
YDL235C	YGL105W	YLL043W	YMR116C	YMR228W	YJR019C	YIR026C	YGR040W	YMR294W	YDL188C	YMR203W	YGL213C	YEL036C	YNL228W
YEL024W	YDR498C	YBR212W	YPL111W	YPR057W	YOR085W	YLR056W	YPR065W	YPL001W	YGR109C	YGR112W	YOL136C	YJL014W	YMR108W
YEL018W	YDL029W	YNL015W	YCL055W	YNR035C	YDL226C	YMR270C	YPR191W	YFL039C	YOL043C	YHR208W	YEL037C	YJL110C	YPL043W
YER161C	YKL081W	YDL075W	YFR025C	YCL032W	YBL016W	YBR018C	YMR139W	YNL307C	YLR291C	YIL136W	YHL022C	YFL056C	YLR153C
YKL193C	YFR053C	YML098W	YLR354C	YIL154C	YBL068W	YBR057C	YPR035W	YGL148W	YDR088C	YOR099W	YHL014C	YJR155W	YPR074C
YPR129W	YFL018C	YOL143C	YPL069C	YBR034C	YHR025W	YER118C	YNL005C	YGL155W	YNR015W	YOR176W	YKR061W	YNL331C	YPL089C

Title: Methods for Selecting Nucleic Acid Probes  
 Inventor: Hubbell  
 Attorney Docket No. 3373.1  
 Sheet 17 of 30

Figure 17

DOT 222" 59654460

# Latin Square Experiment

Groups

Exp

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	0	0.25	0.5	1	2	4	8	16	32	64	128	256	512	1024
2	0.25	0.5	1	2	4	8	16	32	64	128	256	512	1024	0
3	0.5	1	2	4	8	16	32	64	128	256	512	1024	0	0.25
4	1	2	4	8	16	32	64	128	256	512	1024	0	0.25	0.5
5	2	4	8	16	32	64	128	256	512	1024	0	0.25	0.5	1
6	4	8	16	32	64	128	256	512	1024	0	0.25	0.5	1	2
7	8	16	32	64	128	256	512	1024	0	0.25	0.5	1	2	4
8	16	32	64	128	256	512	1024	0	0.25	0.5	1	2	4	8
9	32	64	128	256	512	1024	0	0.25	0.5	1	2	4	8	16
10	64	128	256	512	1024	0	0.25	0.5	1	2	4	8	16	32
11	128	256	512	1024	0	0.25	0.5	1	2	4	8	16	32	64
12	256	512	1024	0	0.25	0.5	1	2	4	8	16	32	64	128
13	512	1024	0	0.25	0.5	1	2	4	8	16	32	64	128	256
14	1024	0	0.25	0.5	1	2	4	8	16	32	64	128	256	512

Figure 18

# Latin Square Data Sets from Yeast\_Test\_Hyb Chips

<i>Lot 1 (9912072)</i>			
No Background:	3 Scans	14 chips	(530, PMT=701; 570, PMT=701; 570, PMT=600)
+ Background:	3 Scans	14 chips	(530, PMT=701; 570, PMT=701; 570, PMT=600)
<i>Lot 2 (9910426)</i>			
No Background:	1 Scan	14 chips	(570, PMT=600)
No Background:	1 Scan	14 chips	(570, PMT=600)
<i>Lot 3 (9910427)</i>			
+ Background:	1 Scan	14 chips	(570, PMT=526)
No Background_Rep1:	1 Scan	14 chips	(570, PMT=526)
No Background_Rep2:	1 Scan	14 chips	(570, PMT=526)
<i>Lot 4 (9913514)</i>			
No Background:	1 Scan	14 chips	(570, PMT=526)
+ Background:	1 Scan	14 chips	(570, PMT=526)
<i>Lot 5 (9914059)</i>			
+ Background_Rep1:	1 Scan	14 chips	(570, PMT=526)
+ Background_Rep2:	1 Scan	14 chips	(570, PMT=526)
No Background:	1 Scan	14 chips	(570, PMT=526)

Figure 19

# Bootstrapping

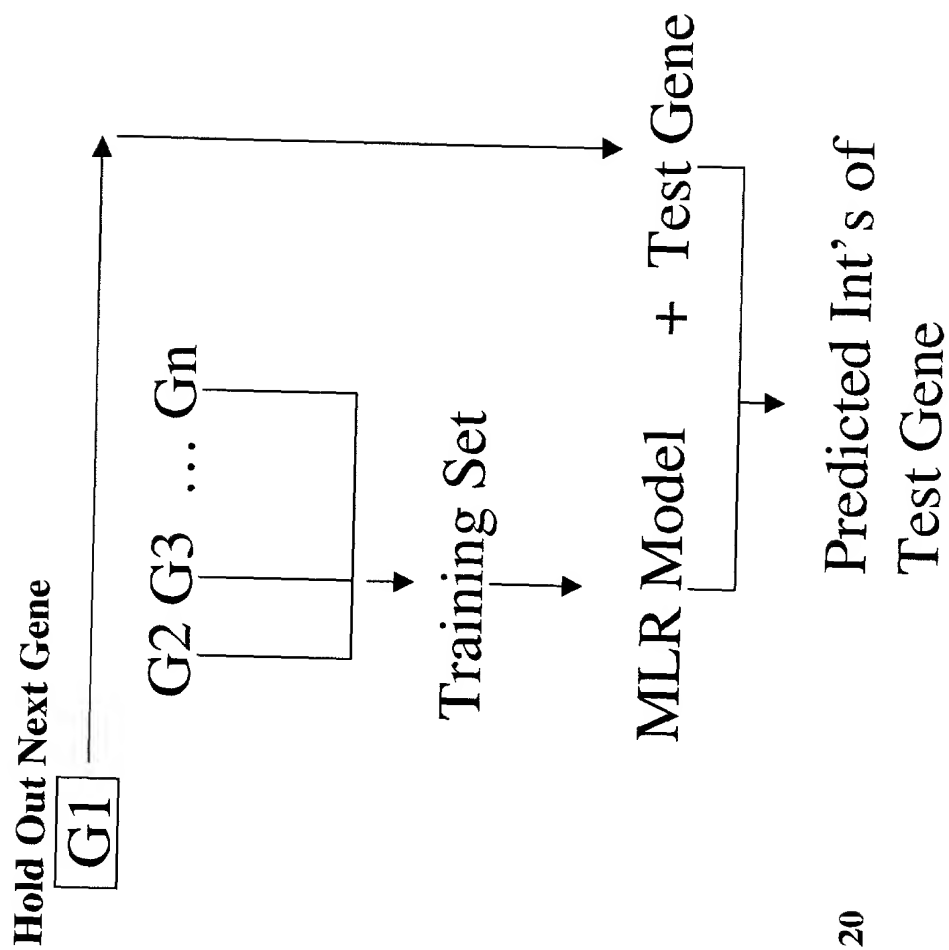
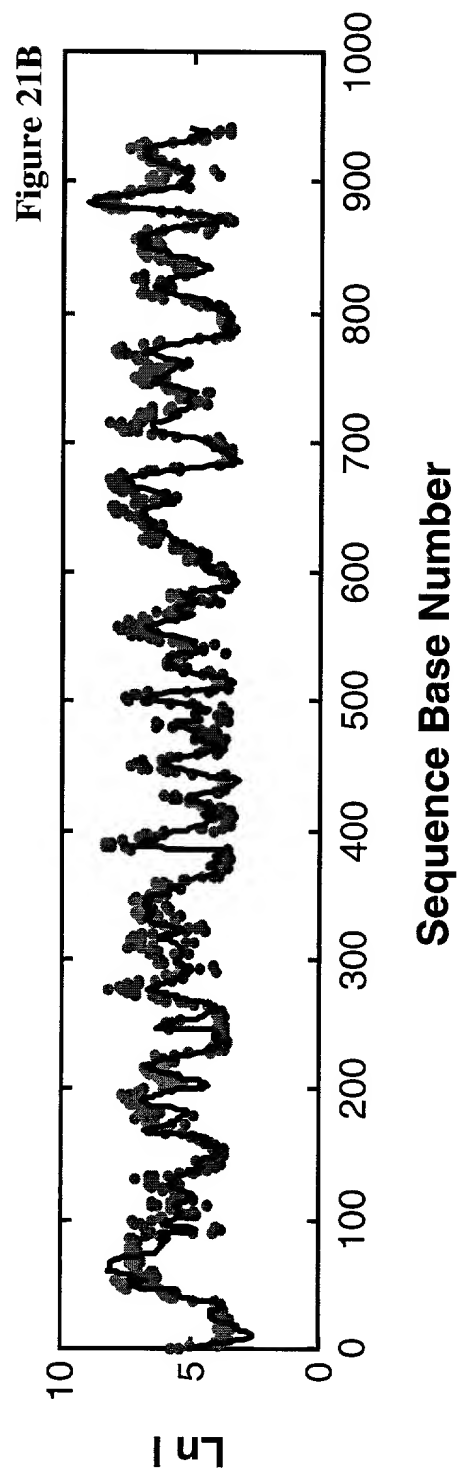
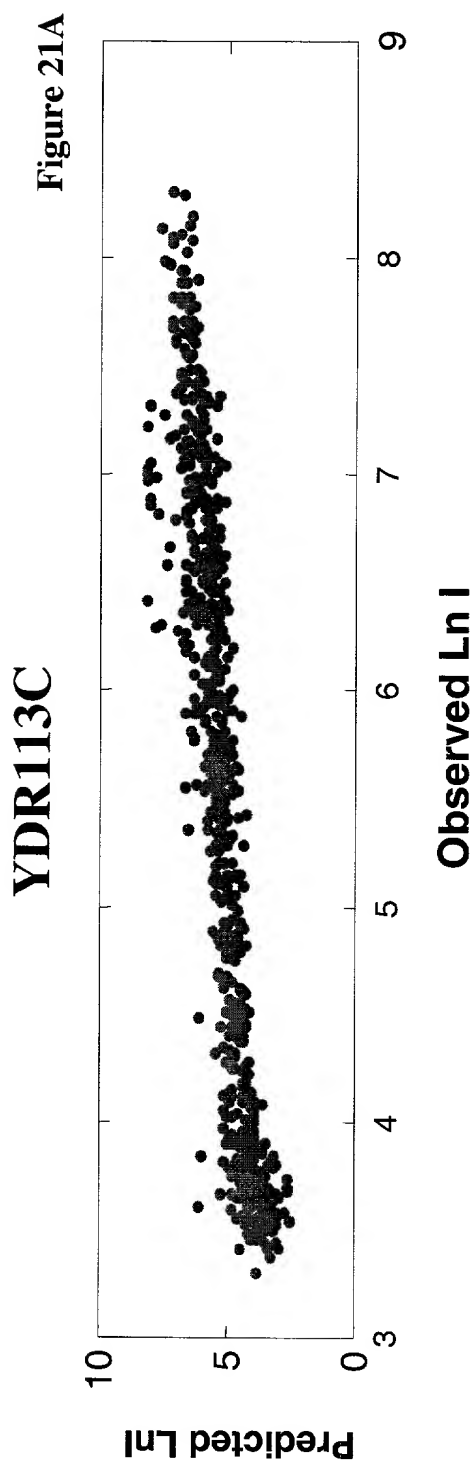


Figure 20



YGR109C

Figure 22A

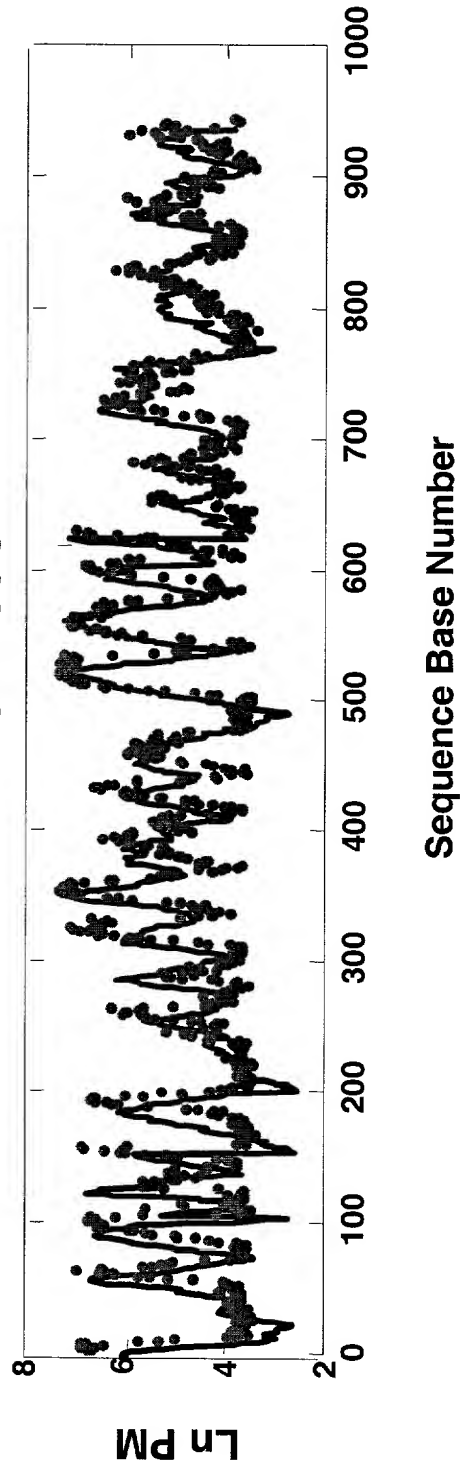
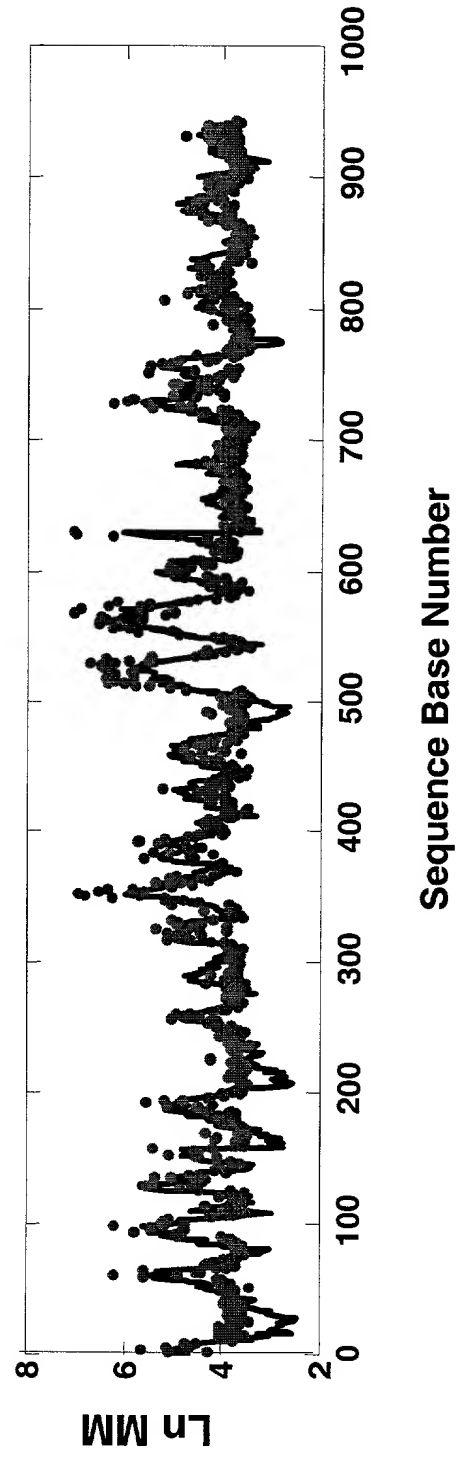


Figure 22B



# Ln(Int) at Different Spike Concentrations

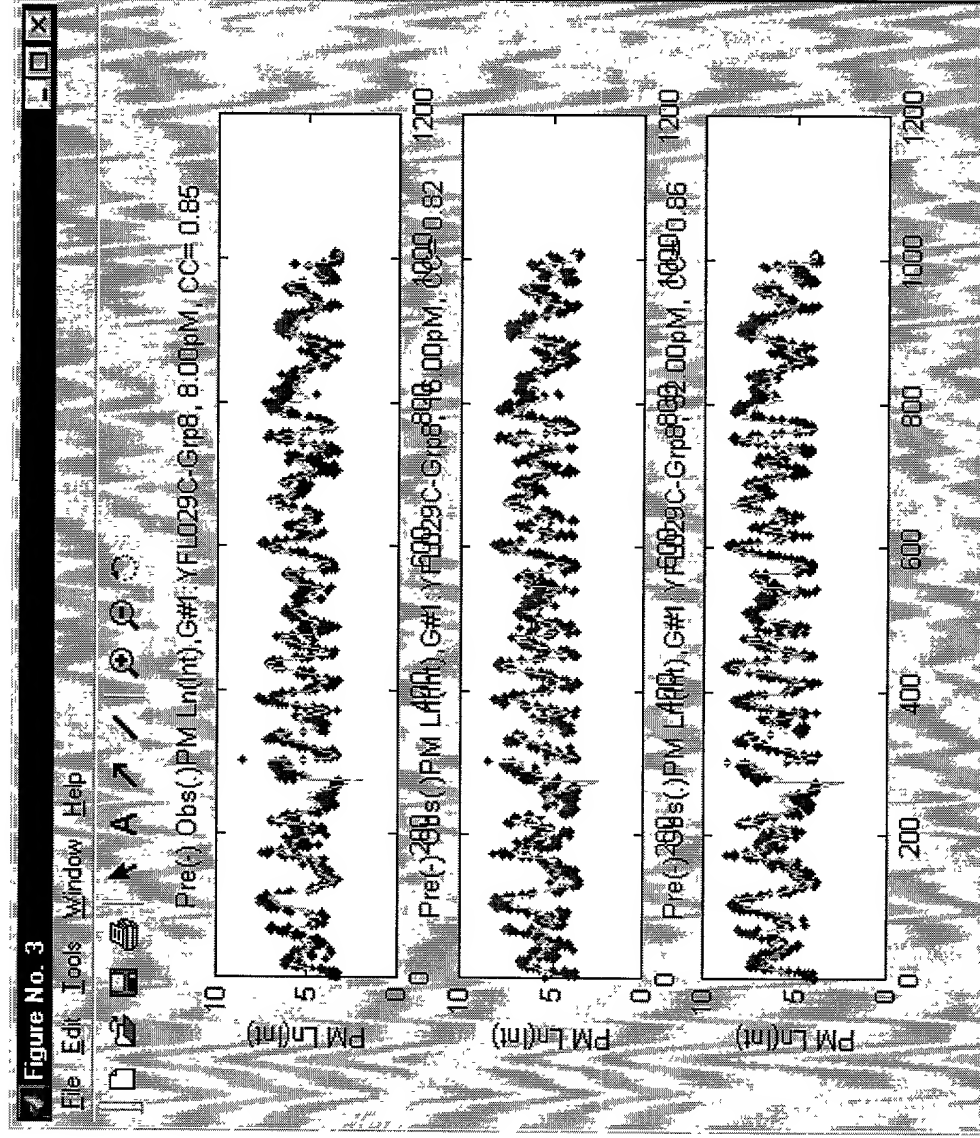


Figure 23

# Correlation between Predicted & Observed $\text{Ln}(\text{Int})$ 's

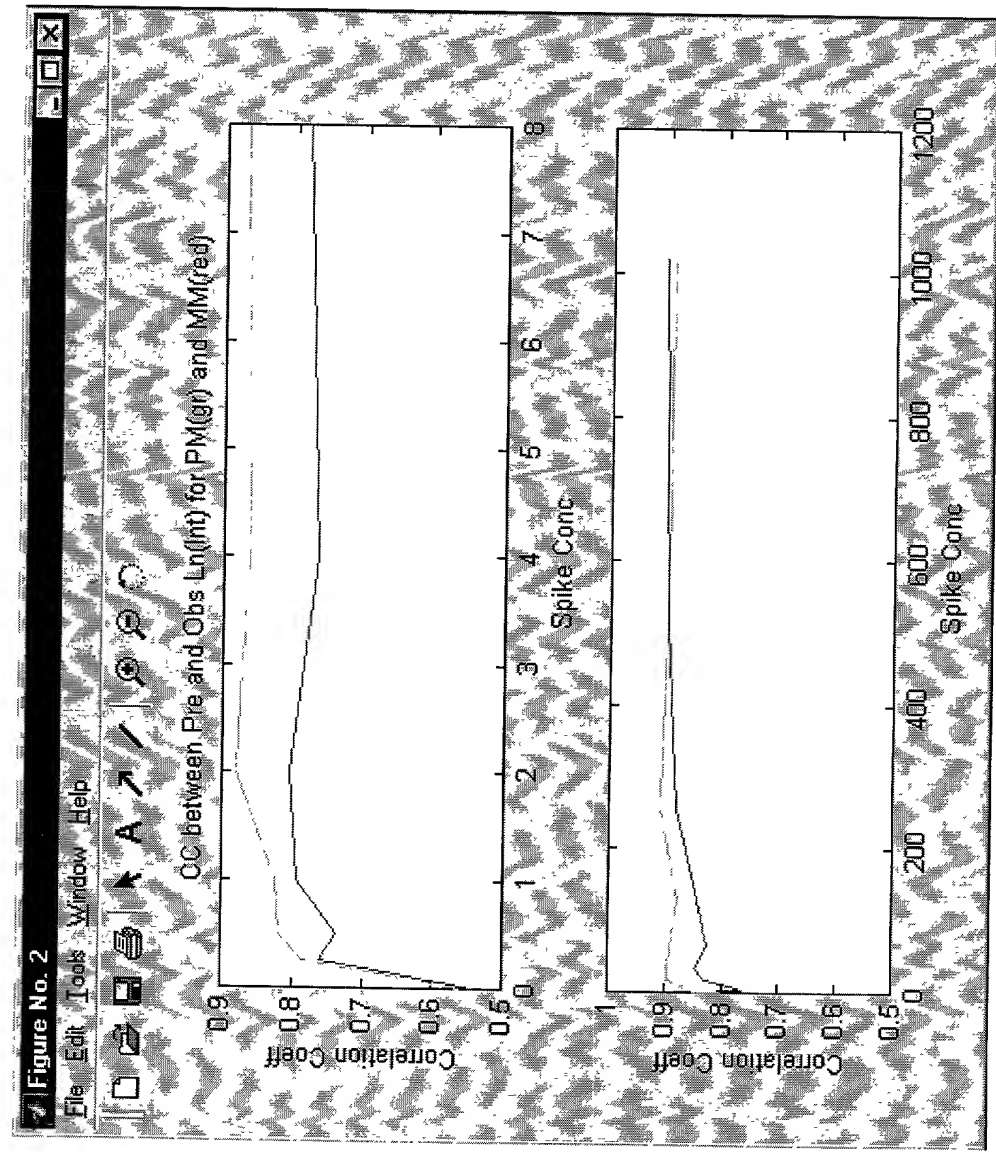


Figure 24

001221" 596514.60



# Negative Control: Gene in Wrong Orientation

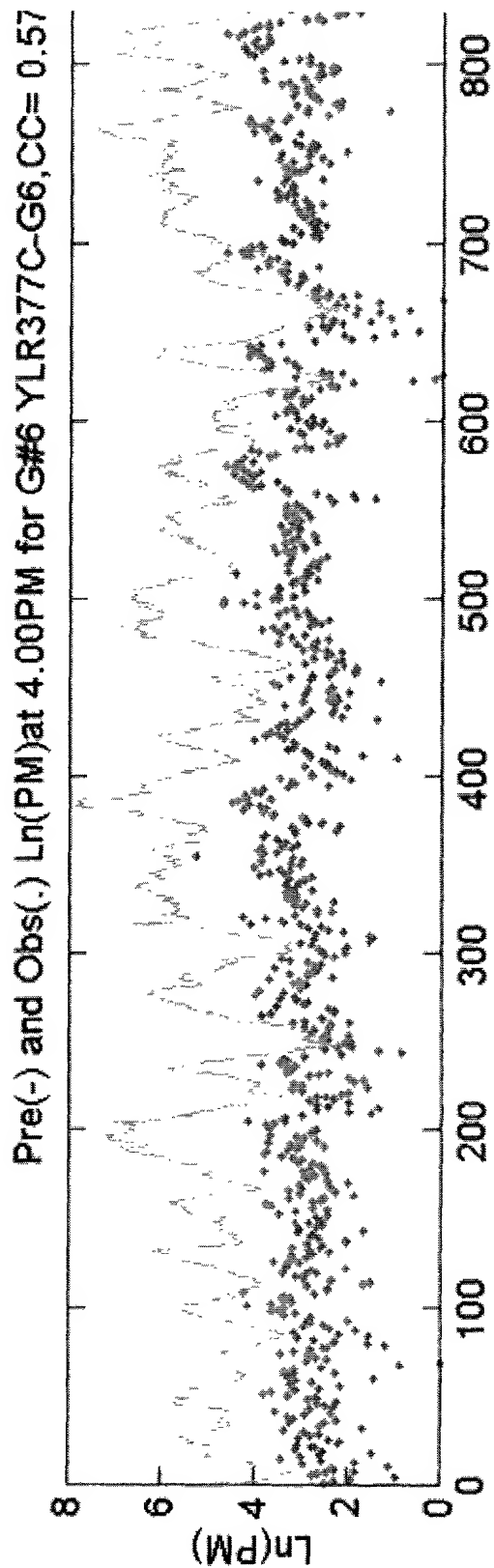


Figure 25

# Predicted Observed Slopes

CC=0.42

CC=0.84

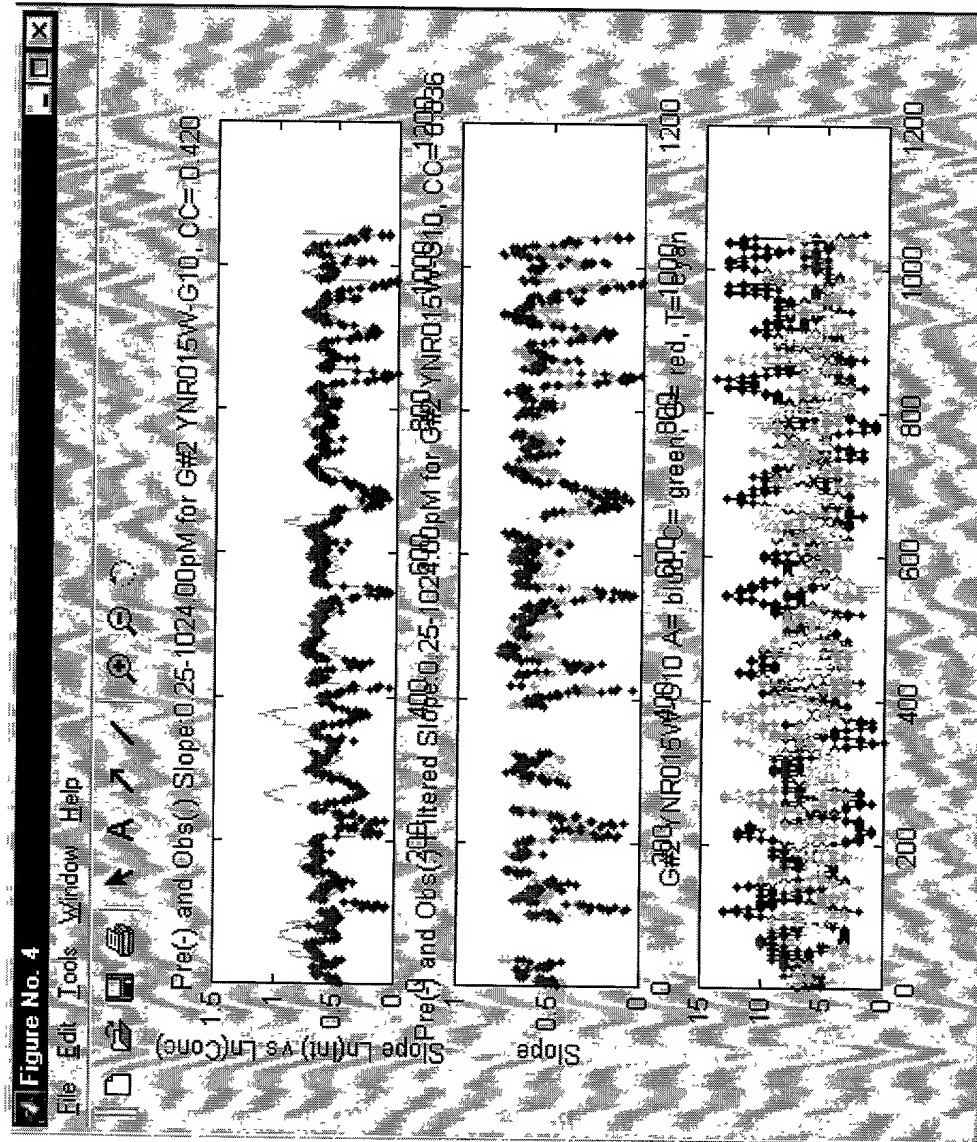
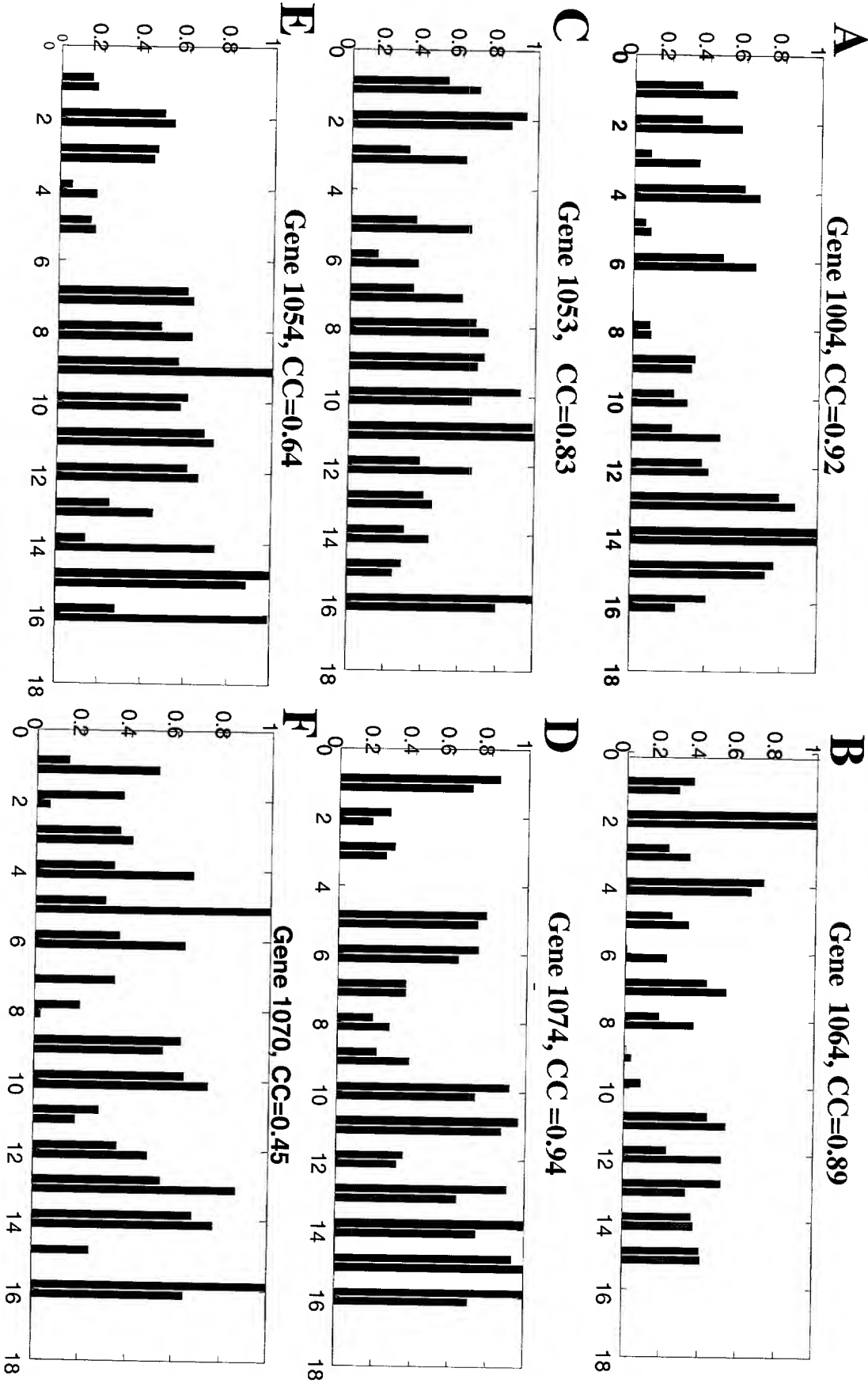


Figure 26

# From Yeast to Human

Figure 27

Using Parameters from Yeast Model System to Predict Human\_U95A



09746365 v. 23.1.00

DOT 227" 59654460

# Predictions for Hu\_U95a Probe Sets

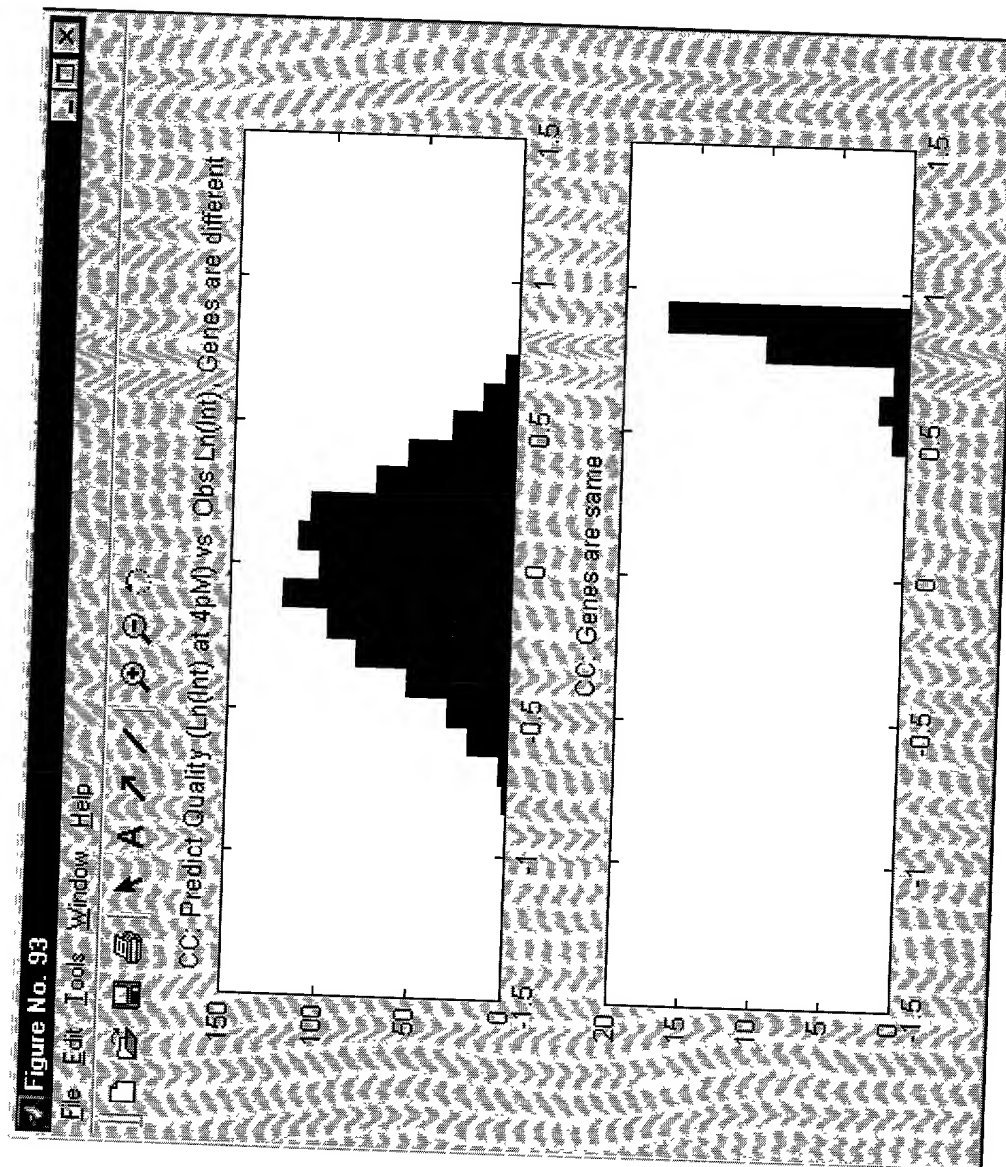


Figure 28

# DOT-2.2T "Selected By Dynamic Sixteen Probes Selected By Dynamic Programming Algorithm

Title: Methods for Selecting Nucleic Acid  
Probes  
Inventor: Hubbell  
Attorney Docket No. 3373.1  
Sheet 29 of 30

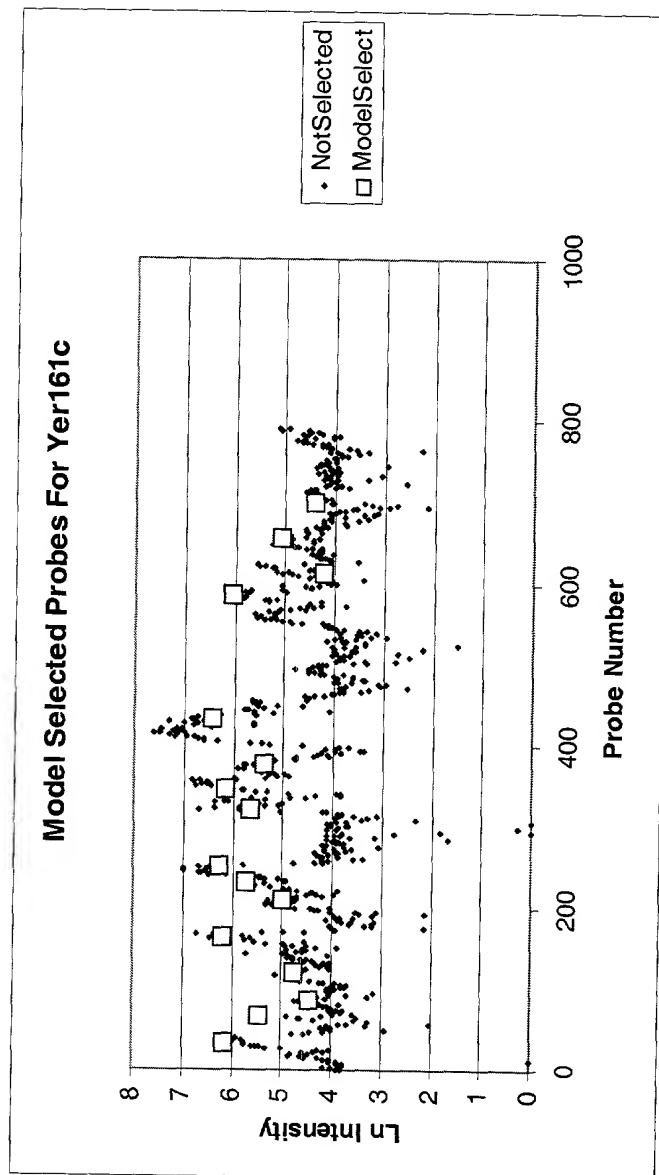


Figure 29

# Comparison of AveDiff Values of all Yeast Test Chip Genes: New vs Random vs Rules Selection

Title: Methods for Selecting Nucleic Acid Probes  
Inventor: Hubbell  
Attorney Docket No. 3373.1  
Sheet 30 of 30

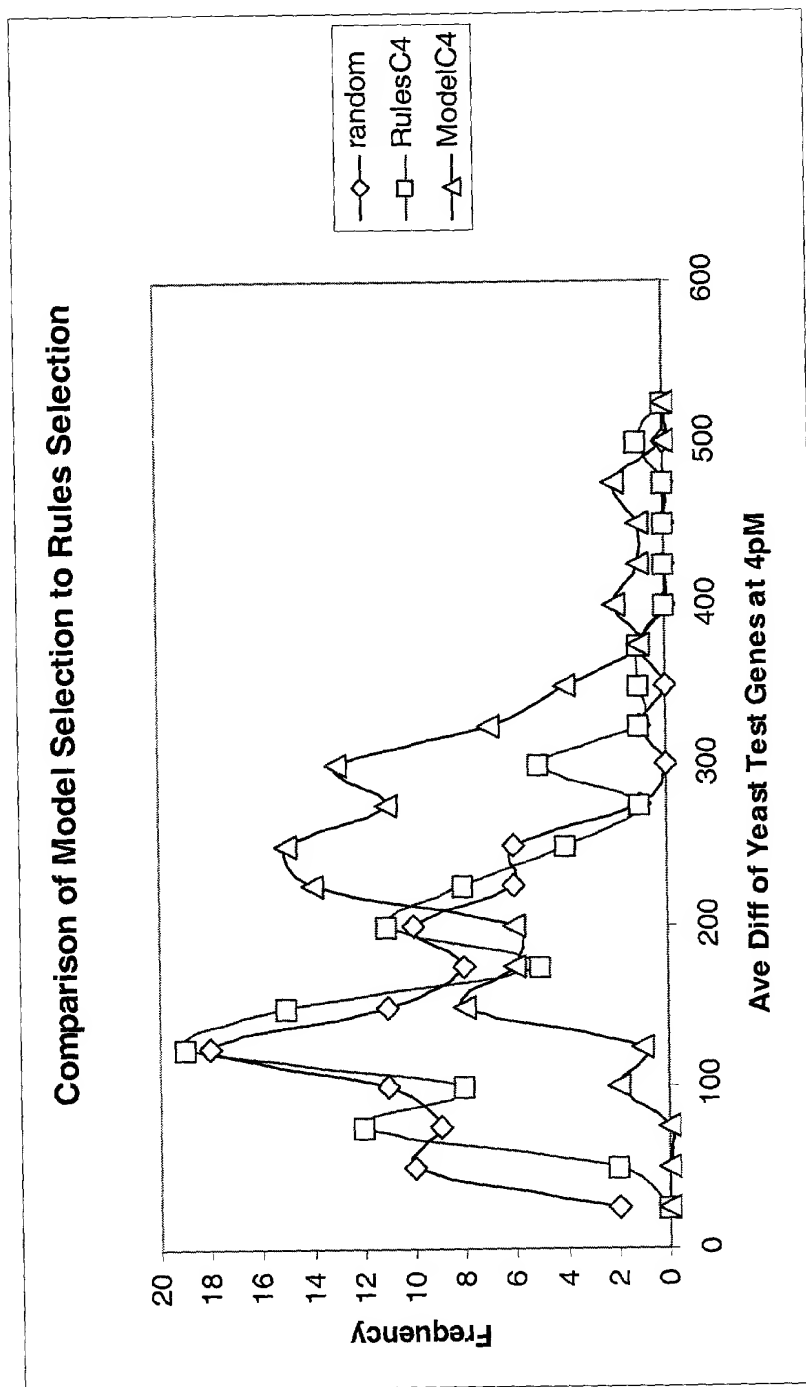


Figure 30